FIG 1A


```
                        5                  10
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
 *                  *                       *   *
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val

                       25                  30
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asn Ser Tyr
                           *   *   *   *   *
Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr

Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr

                       45                  50
Pro Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn
                               *       *       *
Pro Gly Gln Gly Leu Glu Trp Ile Gly Trp Ile Asp
      *                                        CDR
Pro Glu Gln Gly Leu Glu Trp Ile Gly Trp Ile Asp

                       65                  70
Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg
 *   *
Asp Pro Lys The Gln Gly Arg Val Thr Met Thr Arg
                           *   *   *   *       *
Asp Pro Lys Phe Gln Gly Lys Ala Ser Ile Thr Ser

                       85                  90
    Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
 *                          *
Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala

                   105                 110
 -   -   -   -   -   -   -   -   -   -   -   -

Thr Ser Ser Phe Asp Phe Trp Gly Gln Gly Thr Thr
        CDR 3
Thr Ser Ser Phe Asp Phe Trp Gly Gln Gly Thr Thr
          /  J>>
```

FIG. 1B


```
          15                  20
Lys Pro Gly Ala Ser Val Lys Val  Human HV3 VH

Lys Pro Gly Ala Ser Val Lys Val  "CDR Grafted" VH
 *               *           *
Arg Pro Gly Ala Leu Val Lys Leu  Murine 1308F VH

          35                  40
Tyr Met His Trp Val Arg Gln Ala
     *   *
Tyr Ile Tyr Trp Val Arg Gln Ala
    CDR 1                *       *
Tyr Ile Tyr Trp Val Lys Gln Arg

          55                  60
Pro Ser Gly Gly Ser Thr Ser Tyr
     *   *       *       *   *
Pro Glu Asn Gly Asn Thr Val Phe
2
Pro Glu Asn Gly Asn Thr Val Phe

          75                  80
Asp Thr Ser Thr Ser Thr Val Tyr

Asp Thr Ser Thr Ser Thr Val Tyr
               *   *       *
Asp Thr Ser Ser Asn Thr Ala Tyr

          95                  100
Val Tyr Tyr Cys Ala

Val Tyr Tyr Cys Ala Tyr Tyr Gly

Val Tyr Tyr Cys Ala Tyr Tyr Gly
               <<V  /     D
        115
 -   -   -   -   -

Leu Thr Val Ser Ser

Leu Thr Val Ser Ser
```

FIG. 2A


```
                          5                  10
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
          *                               *   *   *
Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Met Tyr

                         25                  30
Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
          *                  *        *   *   *
Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Arg Tyr
                                   CDR 1
Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Arg Tyr

                         45                  50
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser
                                    *       *
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg Ala Asn
          *              *            *
Gly Lys Ser Pro Lys Thr Leu Ile His Arg Ala Asn

                         65                  70
Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr

Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
                                    *       *   *
Arg PHE Ser Gly Ser Gly Ser Gly Gln Glu Tyr Ser

                         85                  90
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn
                                    *       *   *
Asp Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Phe His
  *        *   *   *
Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Phe His

                        105
 -   -   -   -   -   -   -
Gly Thr Lys Leu Glu Ile Lys

Gly Thr Lys Leu Glu Ile Lys
```

FIG. 2B


```
          15                  20
Ala Ser Val GLY Asp Arg Val Thr - Human K102 VL

Ala Ser Val Gly Asp Arg Val Thr - "CDR Grafted" VL
 *       *       *
Val Ser Leu Gly Glu Arg Val Thr -Murine 1308F VL

          35                  40
Leu Ala Trp Tyr Gln Gln Lys Pro
      *
Leu Asn Trp Tyr Gln Gln Lys Pro
                  *
Leu Asn Trp Phe Gln Gln Lys Pro

          55                  60
Ser Leu Glu Ser Gly Val Pro Ser
 *       *   *
Arg Leu Val Asp Gly Val Pro Ser
 CDR 2
Arg Leu Val Asp Gly Val Pro Ser

          75                  80
Leu Thr Ile Ser Ser Leu Gln Pro

Leu Thr Ile Ser Ser Leu Gln Pro
                              *
Leu Thr Ile Ser Ser Leu Glu Phe

          95                  100
Ser Tyr Ser  -   -   -
 *   *   *
Glu Phe Pro Tyr Thr Phe Gly Gly
  CDR 3
Glu Phe Pro Tyr Thr Phe Gly Gly
       <<V / J>>
```

FIG. 3A

FIG. 3B

```
  ProLysPheGlnGlyArgValThrNetThrArgAspThrSerThrSerThrValTyr Met
  CCGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATG
241--------+---------+---------+---------+---------+---------+
  GGCTTCAAGGTCCCGTCTCAGTGGTACTGGTCCCTGTGCAGGTGCTCGTGTCAGATGTAC

  GluLeuSerSerLeuArgSerGluAspThrAlaValTyrTyrCysAlaTyrTyrGlyThr
  GAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGTACTACGGTACA
301--------+---------+---------+---------+---------+---------+
  CTCGACTCGTCGGACTCTAGACTCCTGTGCCGGCACATAATGACACGCATGATGCCATGT

  SerSerPheAspPheTrpGlyGlnGlyThrThrLeuThrValSerSer
  AGCTCCTTTGACTTCTGGGGCCAAGGCACCACTCTCACAGTGAGCTCA
361--------+---------+---------+---------+--------

  TCGAGGAAACTGAAGACCCCGGTTCCGTGGTGAGAGTGTCACTCGAGTattcctagg 5'
                                    ggtgagagtgtcactcgagtattcctagggc
                                  3'                               5'
```

FIG. 4A

```
cgcggatccatggacatgagggtcccc
          MetAspMepArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuProGlyAla
        ccATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCC
      1 ---------+---------+---------+---------+---------+---------+---------+
        TACCTGTACTCCCAGGGGCGAGTCGAGGACCCCGAGGACGACGAGACCGAGGGTCCACGG

          LysCysAspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArg
          AAATGTGATATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGA
     61 ---------+---------+---------+---------+---------+---------+---------+
          TTTACACTATAGGTCTACTGGGTCAGAGGAAGGTGGGACAGACGTAGACATCCTCTGTCT

          ValYhrIleThrCysLysAlaSerGlnAspIleAsnArgTyrLeuAsnTrpTyrGlnGln
          GTCACCATCACTGGCAAGGCGAGTCAGGACATTAATAGGTAGTTAAACTGGTACCAGCAG
    121 ---------+---------+---------+---------+---------+---------+---------+
          CAGTGGTAGTGAACGTTCCGCTCAGTCCTGTAATTATCCATAAATTTGACCATGGTCGTC

          LysProGlyLysAlaProLysLeuLeuIleTyrArgAlaAsnArgLeuValAspGlyVal
          AAACCCGGGAAAGCCCCTAAGCTCCTGATCTATCGTGCAAACAGATTGGTAGATGGGGTC
    181 ---------+---------+---------+---------+---------+---------+---------+
          TTTGGGCCCTTTCGGGGATTCGAGGACTAGATAGCACGTTTGTCTAACCATCTACCCCAG
```

7 / 17

FIG. 4B

```
    ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeu
    CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTG
241 ---------+---------+---------+---------+---------+---------+
    GGTAGTTCCAAGTCGCCGTCACCTAGACCCTGTCTTAAGTGAGAGTGTTAGTCGTCGGAC

    GlnProAspAspPheAlaThrTyrTyrCysLeuGlnPheHisGluPheProTyrThrPhe
    CAGCCTGATGATTTTGCAACTTATTACTGCCTACAGTTTCATGAGTTTCCGTACACGTTC
301 ---------+---------+---------+---------+---------+---------+
    GTCGGACTACTAAAACGTTGAATAATGACGGATGTCAAAGTACTCAAAGGCATGTGCAAG
                                                      3' gtgcaag

    GlyGlyGlyThrLysLeuGluIleLys
    GGAGGGGGGACCAAGCTTGAAATAAAA 3'
361 ---------+---------+-------

    CCTCCCCCCCTGGTTCGAACTTTATTTT 5'
    cctccccccctggttcgaaccc 5'
```

8 / 17

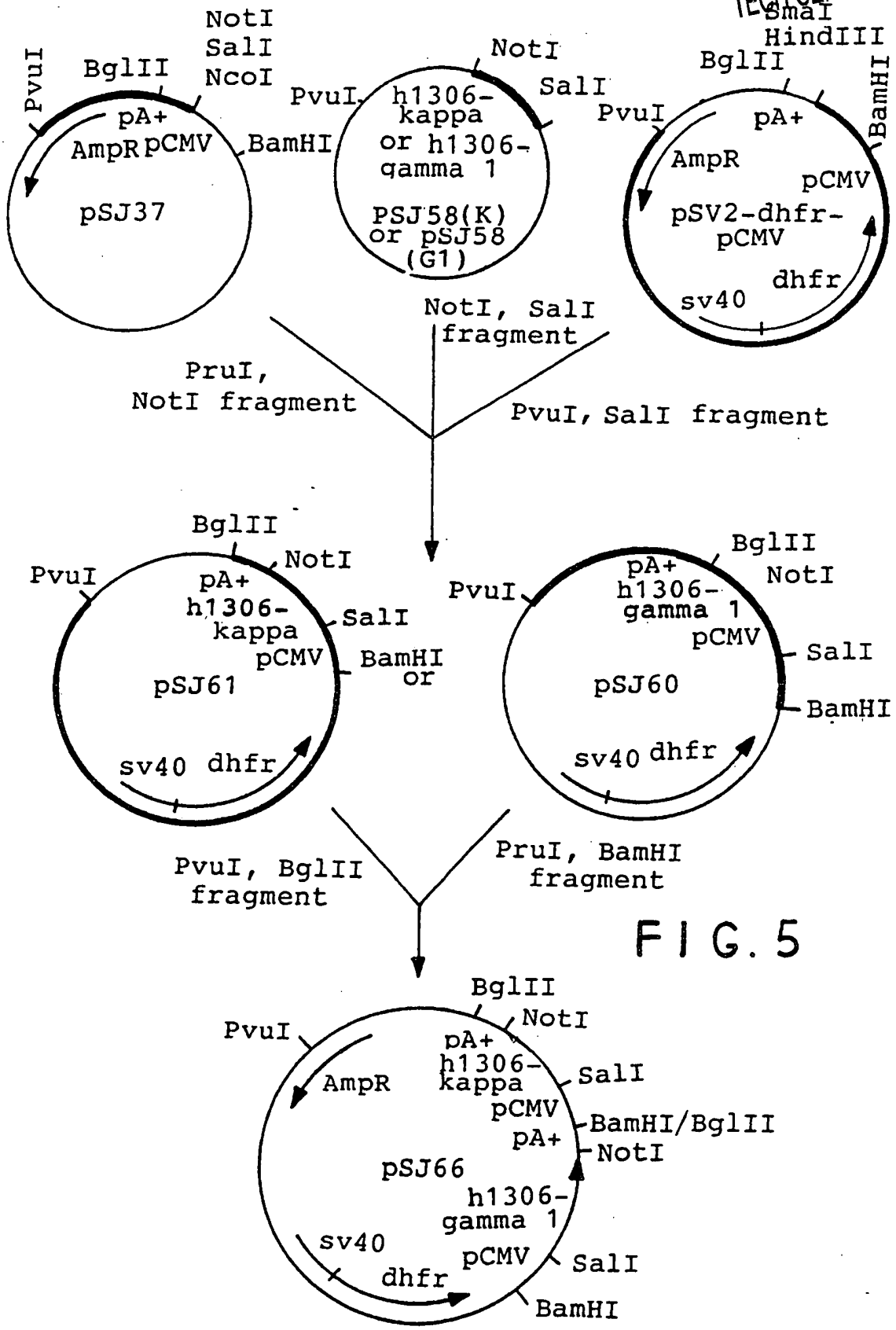

FIG. 5

FIG. 6

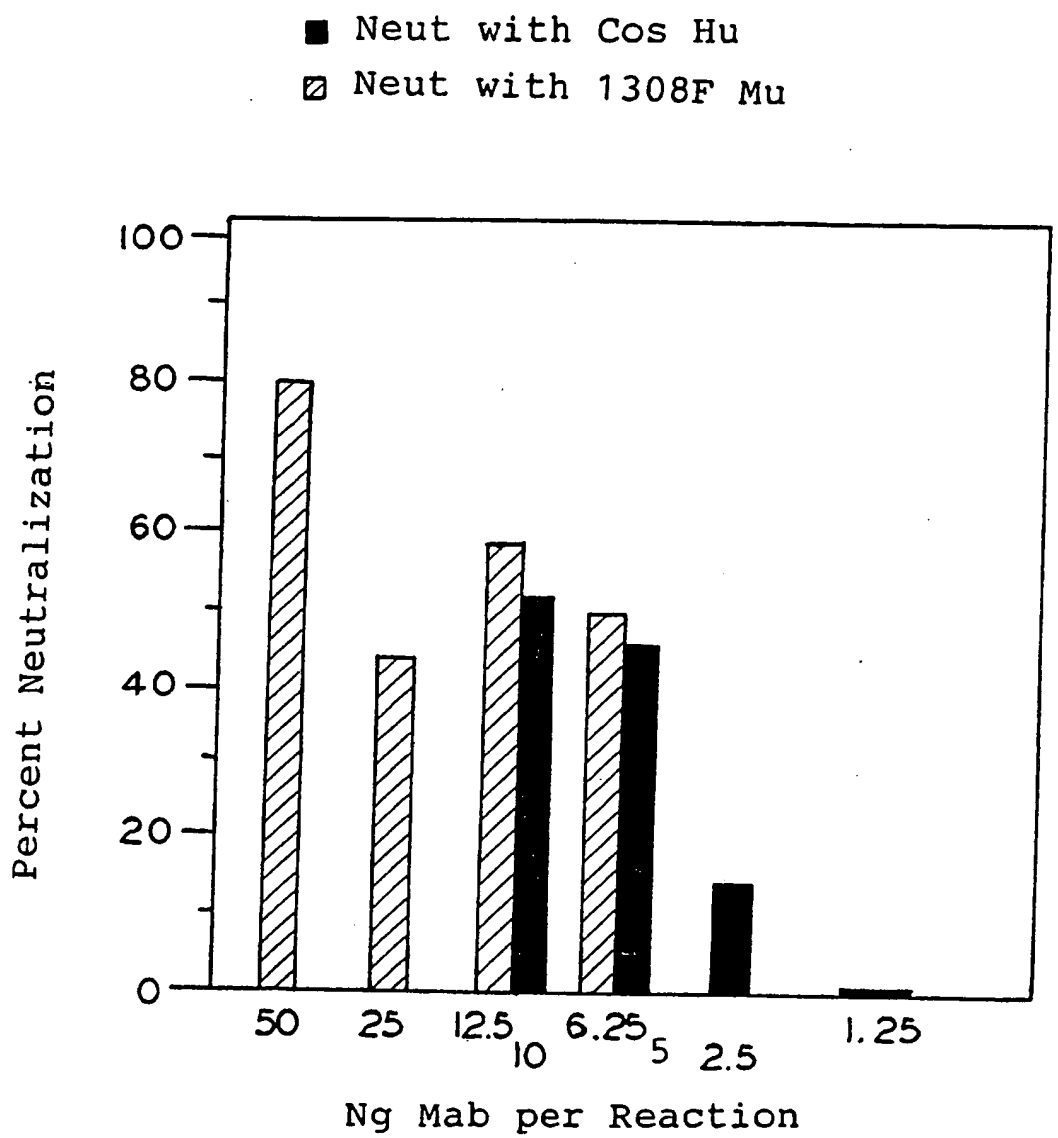

FIG. 7A

```
                5                  10                  15
    Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Human VH (Cor)
 1  Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr "Humanized" VH
                    *                  *   *   *   *
    Gln Val Glu Leu Gln Glu Ser Gly Pro Gly Ile Leu Gln Pro Ser Murine 1129 VH

    Gln Yhr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser
16  Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser
                *
    Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser

    Ser Ser Gly Met Cys Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
     *              *
31  Thr Ser Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
                                                *           *
    Thr Ser Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Glu

    Ala Leu Glu Trp Leu Ala Asp Ile Glu Trp Asp Asp Asp Lys Asp
                                       *           *
46  Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp
     *
    Gly Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp
```

FIG. 7B

```
    Tyr Asn Thr Ser Leu Asp Thr Arg Leu Thr Ile Ser Lys Asp Thr
              *              *   *
61  Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr

    Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr


    Swe Lys Asn Gln Val Val Leu Thr Val Thr Asn Met Asp Pro Ala
                                   *
76  Ser Lys Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala
         *                   *         *         *           *
    Ser Ser Asn Gln Val Phe Leu Lys Ile Thr Gly Val Asp Thr Ala


    Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ile Yhr Val Ile Pro Ala Pro Ala Gly
                                        *   *   *   *   *
91  Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp

    Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp


    Tyr Met Asp Val Trp Gly Arg Gly Thr Pro Val Thr Val Ser Ser
         *                   *         *
106 Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser

    Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
```

12/17

FIG. 8A

```
                    5                  10                  15
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val  - Human K102 VL
                                                               (SEQ ID 33)
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val  - "CDR Grafted" VL
                *                   *   *   *               *   (SEQ ID 34)
Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro  - Murine 1129 VL
                                                               (SEQ ID 35)
                   20                  25                  30
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser
                                *   *   *   *       *   *
Gly Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly
      *   *             *         *   *   *   *  CDR 1
Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Gly

                   35                  40                  45
Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 *   *   *
Tyr Met His  -  Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys

Tyr Met His  -  Trp Tyr Gln Gln Lys Ser Ser Thr Ser Pro Lys

                   50                  55                  60
Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser
      *             *       *       *
Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser
                          CDR 2
Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Gly
```

FIG. 8B

```
                    65                  70                  75
Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile

Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
                                    *   *   *   *
Arg Phe Ser Gly Ser Gly Ser Gly Asn Ser Tyr Ser Leu Thr Ile

                    80                  85                  90
Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln

Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln
          *       *   *       *
Ser Ser Ile Gln Ala Glu Asp Val Ala Thr Tyr Tyr Cys Phe Gln

                    95                  100                 105
Tyr Asn Ser Tyr Ser
 *   *   *       *
Gly Ser Gly Tyr Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
          CDR 3
Gly Ser Gly Tyr Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

                <<V / ]>>
```

FIG. 9A

```
SJ153  5'-GGCGTCGACTCACC-
       ATGGACTGGACCTGGAGGGTCTTCTGCTTGCTGGCTGTAGCACCAGGTGCCCACTCCC-3'
                                                          SJ150 5'-CCAG
    1 ---------+---------+---------+---------+---------+---------+ 60

      MetAspTrpThrTrpArgValPheCysLeuLeuAlaValAlaProGlyAlaHisSerGln

      GTCACCTTAAGGGAGTCTGGTCCTGCCCTGGTGAAACCCACACAGACCCTCACACTGACC
   61 ---------+---------+---------+---------+---------+---------+ 120
                                                3'-GGAGTGTGACTGG

      ValThrLeuArgGluSerGlyProAlaLeuValLysProThrGlnThrLeuThrLeuThr

      TGCACC-3'
                                                     SJ151 5'- CAG
  121 ---------+---------+---------+---------+---------+---------+ 180
      ACGTGGAAGAGACCCAAAAGTGACTCGTGAAGACCATACTCACATCCGACCTAAGCAGTC

      CysThrPheSerGlyPheSerLeuSerThrSerGlyMetSerValGlyTrpIleArgGln

      CCCCCAGGGAAGGCCCTGCACTCGCTTGCAGACATTTGGTGGGATGACAAAAAGGACTAT
  181 ---------+---------+---------+---------+---------+---------+ 240
      GGGGGTCCCTTCCGGG-5' SJ149                          3'- GATA

      ProProGlyLysAlaLeuGluTrpLeuAlaAspIleTrpTrpAspAspLysLysAspTyr
```

FIG. 9B

```
    AATCCATCCCTGAAG-3'
                                                          SJ152 5'-GGTC
241 ---------+---------+---------+---------+---------+---------+ 300
    TTAGGTACCGACTTCTCGGCCGAGTGTTAGAGGTTCCTATGGAGGTTTTTGGTCCACCAG

    AsnProSerLeuLysSerArgLeuThrIleGerLysAspThrSerLysAsnGlnValVal


    CTTAAAGTGACCAACATGGACTCCTGCTGATACTGCCACTTACTACTGTGCTCGGTCTATG
301 ---------+---------+---------+---------+---------+---------+ 360
    GAATTTCACTGGTTG-5' SJ148                                3'-TAC

    LeuLysValThrAsnMetAspProAlaAspThrAlaThrTyrTyrCysAlaArgSerMet


361 ---------+---------+---------+---------+---------+---------+ 417
    TAGTGCTTGACCATGAAGCTACAGACCCCGCCGCCCTGGTGCCAGTGGCACTCGAGTCCG-5' SJ147

    IleThrAsnTrpTyrPheAspValTrpGlyAlaGlyThrThrValThrValSerSer
```

FIG. 10